**Supplementary file 6: Software used in this study.**

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| Program / library / script | Package | Source |
| Oufti | www.oufti.org | (Paintdakhi et al., 2016) |
| MATLAB | www.mathworks.com | Mathworks |
| Python | www.python.org | Python Software Foundation |
| Numpy | www.numpy.org | (Harris et al., 2020) |
| Scipy | www.scipy.org | (Virtanen et al., 2020) |
| Pytorch | www.pytorch.org | (Paszke et al., 2019) |
| Scikit-image | www.scikit-image.org | (Van Der Walt et al., 2014) |
| Scikit-learn | www.scikit-learn.org/stable/ | (Pedregosa et al., 2012) |
| Statsmodels | www.statsmodels.org/stable/index.html | (Seabold and Perktold, 2010) |
| Shapely | www.pypi.org/project/shapely/ | (Gillies, Sean et al., 2023) |
| Matplotlib | www.matplotlib.org | (Hunter, 2007) |
| Seaborn | www.seaborn.pydata.org | (Waskom, 2021) |
| Pandas | www.pandas.pydata.org | (McKinney, 2010) |
| Python | Omnipose neural network | (Cutler et al., 2022) |
| MATLAB | SuperSegger | (Stylianidou et al., 2016) |
| Python | Unet neural network | (Wiktor et al., 2021; Zhou et al., 2020) |
| snapshots\_analysis\_UNET\_ghv.py | Snapshot image analysis (from UNET masks) – custom Python class | This study  ([www.github.com/JacobsWagnerLab/published/tree/master/Papagiannakis\_2025](https://github.com/JacobsWagnerLab/published/tree/master/Papagiannakis_2025)) |
| snapshots\_analysis\_OUFTI\_GrayGovers\_ghv.py | Snapshot image analysis (from Oufti masks) – custom Python class | This study  ([www.github.com/JacobsWagnerLab/published/tree/master/Papagiannakis\_2025](https://github.com/JacobsWagnerLab/published/tree/master/Papagiannakis_2025)) |
| snapshots\_analysis\_functions.py | Extraction of fluorescence and morphology statistics from cell snapshots – custom Python functions | This study  ([www.github.com/JacobsWagnerLab/published/tree/master/Papagiannakis\_2025](https://github.com/JacobsWagnerLab/published/tree/master/Papagiannakis_2025)) |
| microfluidics\_segmentation\_ghv.py | Cell segmentation and tracking from time-lapse images in microfluidics – custom Python class | This study  ([www.github.com/JacobsWagnerLab/published/tree/master/Papagiannakis\_2025](https://github.com/JacobsWagnerLab/published/tree/master/Papagiannakis_2025)) |
| microfluidics\_analysis\_functions\_ghv.py | Extraction of fluorescence and morphology statistics from time-lapse images in microfluidics – custom Python functions | This study  ([www.github.com/JacobsWagnerLab/published/tree/master/Papagiannakis\_2025](https://github.com/JacobsWagnerLab/published/tree/master/Papagiannakis_2025)) |
| Omnipose\_to\_python\_ghv.py | Extraction of segmentation masks and tracked lineages from Omnipose/SuperSegger to Python for further analysis | This study  ([www.github.com/JacobsWagnerLab/published/tree/master/Papagiannakis\_2025](https://github.com/JacobsWagnerLab/published/tree/master/Papagiannakis_2025)) |
| Otsu\_phase\_segmentation\_ghv.py | Cell segmentation and tracking using Otsu thresholding (Otsu, 1979) | This study  ([www.github.com/JacobsWagnerLab/published/tree/master/Papagiannakis\_2025](https://github.com/JacobsWagnerLab/published/tree/master/Papagiannakis_2025)) |
| LoG\_adaptive\_image\_filter.py | Image filter that applies relative and local thresholding to segment fluorescence objects and particles | This study  ([www.github.com/JacobsWagnerLab/published/tree/master/Papagiannakis\_2025](https://github.com/JacobsWagnerLab/published/tree/master/Papagiannakis_2025)) |
| Microfluidics\_segmentation\_and\_tracking\_example.pdf | Example for cell segmentation and tracking in microfluidics | This study  ([www.github.com/JacobsWagnerLab/published/tree/master/Papagiannakis\_2025](https://github.com/JacobsWagnerLab/published/tree/master/Papagiannakis_2025)) |
| Analysis\_of\_cell\_morphology\_and\_fluorescence\_in\_microfluidics.pdf | Example for the extraction of fluorescence and morphology statistics from time-lapse images in microfluidics | This study  ([www.github.com/JacobsWagnerLab/published/tree/master/Papagiannakis\_2025](https://github.com/JacobsWagnerLab/published/tree/master/Papagiannakis_2025)) |
| Analysis\_of\_cell\_morphology\_and\_fluorescence\_in\_agarose\_pads.pdf | Example for the extraction of fluorescence and morphology statistics from cell snapshots | This study  ([www.github.com/JacobsWagnerLab/published/tree/master/Papagiannakis\_2025](https://github.com/JacobsWagnerLab/published/tree/master/Papagiannakis_2025)) |
| Example\_of\_using\_Otsu\_based\_segmentation\_ghv.pdf | Example for the segmentation of antibiotic-treated cells using the Otsu threshold | This study  ([www.github.com/JacobsWagnerLab/published/tree/master/Papagiannakis\_2025](https://github.com/JacobsWagnerLab/published/tree/master/Papagiannakis_2025)) |
| tune\_diffusion.ipynb | Simulations of the minimal reaction-diffusion model that describes nucleoid segregation in *E. coli*. | This study  (https://github.com/qiweiyuu/polysome) |
| Time\_lapse\_on\_agarose\_pad | Python repository that includes the *fluorescence\_analysis* class and its associated functions, used to track cell trajectories and analyze their fluorescence statistics in time-lapse images on agarose pads. | This study  (https://github.com/alexSysBio/Time\_lapse\_on\_agarose\_pad) |
| flowio\_to\_pandas | Python repository that includes the *flow\_cytometry\_class* class and its associated functions, used to parse FCS files into Pandas. This class can also be used for polygon and histogram gating. | This study  (https://github.com/alexSysBio/flowio\_to\_pandas) |
| nd2\_to\_array.py | Function used to parse .nd2 files into numpy arrays. | This study  (https://github.com/alexSysBio/Adding\_ND2\_images\_to\_python) |
| Bivariate\_medial\_axis\_estimation.py | Functions used to draw the medial axis in segmented cell masks from snapshots or time-lapse images on agarose pads. | This study  (https://github.com/alexSysBio/Cell\_medial\_axis\_definitions) |
| Unever\_background\_correction.py | Functions used to subtract the background from agarose-pad images. | This study  (https://github.com/alexSysBio/Image\_background\_subtraction) |